IN THE CLAIMS

Kindly enter the following amended claims.

1. (Previously presented) A method for determining total nucleic acid in a sample, which comprises:

a) mixing at least one random primer at least 4 nucleotides in length, having at least one detectable species with a sample which may contain nucleic acid,

b) adding at least one nucleotide triphosphate having at least one binding species and optionally at least one second nucleotide triphosphate,

c) adding at least one nucleic acid polymerase,

d) incubating the mixture of step c), under conditions which allow said at least one nucleic acid polymerase to be active,

e) contacting the mixture of step d) with at least one solid phase,

f) measuring total nucleic acid in said sample by measuring the total amount of said at least one detectable species bound to said solid phase, and

g) determining whether the total nucleic acid in said sample is higher or lower than a threshold amount of contamination, wherein the threshold amount of contamination is equal to or less than 100 pg.

2. (Previously presented) A method for determining total nucleic acid in a sample, which comprises:

a) mixing at least one random primer at least 4 nucleotides in length, having at least one binding species with a sample which may contain nucleic acid,

b) adding at least one nucleotide triphosphate having at least one detectable species and optionally at least one second nucleotide triphosphate,

c) adding at least one nucleic acid polymerase,

d) incubating the mixture of step c), under conditions which allow said at least one nucleic acid polymerase to be active,

e) contacting the mixture of step d) with at least one solid phase,

f) measuring total nucleic acid in said sample by measuring the total amount of said at least one detectable species bound to said solid phase, and

g) determining whether the total nucleic acid in said sample is higher or lower than a threshold amount of contamination, wherein the threshold amount of contamination is equal to or less than 100 pg.

3. (Previously presented) A method for determining total nucleic acid in a sample, which comprises:

a) mixing at least one random primer at least 4 nucleotides in length with a sample which may contain nucleic acid,

b) adding at least one nucleotide triphosphate having at least one binding species and optionally at least one nucleotide triphosphate having at least one detectable species and optionally at least one second nucleotide triphosphate,

c) adding at least one nucleic acid polymerase,

d) incubating the mixture of step c), under conditions which allow said at least one nucleic acid polymerase to be active,

e) contacting the mixture of step d) with at least one solid phase,

f) measuring total nucleic acid in said sample by measuring the total amount of said at least one detectable species or the amount of said at least one binding species bound to said solid phase, and

g) determining whether the total nucleic acid in said sample is higher or lower than a threshold amount of contamination, wherein the threshold amount of contamination is equal to or less than 100 pg.

4. (Previously presented) A method for determining total nucleic acid in a sample, which comprises:

a) mixing at least one first labeled random primer at least 4 nucleotides in length having at least one binding species and at least one second random primer at least 4 nucleotides in length having at least one detectable species, with a sample which may contain nucleic acid,

b) adding at least one nucleic acid ligase,

c) incubating the mixture of step b), under conditions which allow said at least one nucleic acid ligase to be active,

d) contacting the mixture of step c) with at least one solid phase,

e) measuring total nucleic acid in said sample by measuring the total amount of said at least one detectable species or the amount of said at least one binding species bound to said solid phase, and

f) determining whether the total nucleic acid in said sample is higher or lower than a threshold amount of contamination, wherein the threshold amount of contamination is equal to or less than 100 pg.

5. (Previously presented) A method for determining total nucleic acid in a sample, which comprises:

a) mixing at least one first labeled random primer at least 4 nucleotides in length having at least one binding species and at least one second random primer at least 4 nucleotides in length having at least one detectable species, with a sample which may contain nucleic acid,

b) adding at least one nucleic acid ligase and at least one nucleic acid polymerase,

c) incubating the mixture of step b), under conditions which allow said at least one nucleic acid ligase and at least one nucleic acid polymerase to be active,

d) contacting the mixture of step c) with at least one solid phase,

e) measuring total nucleic acid in said sample by measuring the total amount of said at least one detectable species or the amount of said at least one binding species bound to said solid phase, and

f) determining whether the total nucleic acid in said sample is higher or lower than a threshold amount of contamination, wherein the threshold amount of contamination is equal to or less than 100 pg.

6. (Previously presented) A method as in claim 1, wherein said at least one binding species is selected from the group consisting of biotin, avidin, streptavidin, antibody,

antigen, lectin, receptor, ligand, hormone, nucleic acid sequence, mimitope and nucleic acid base pairing polymer.

7. (Previously presented) A method as in claim 1, wherein said at least one detectable species is selected from the group consisting of biotin, avidin, streptavidin, antibody, antigen, lectin, receptor, ligand, hormone, nucleic acid sequence, mimitope, nucleic acid base pairing polymer, fluorescent molecule, electrochemiluminescent molecule, radioactive molecule, colored molecule, peroxidase, alkaline phosphatase and enzymes capable of producing a detectable species.

8. (Previously presented) A method as in claim 1, wherein said at least one nucleic acid polymerase is selected from the group consisting of Taq DNA polymerase, T4 DNA polymerase, Klenow fragment, Pfu DNA polymerase, Exo- Pfu DNA polymerase, E. coli DNA polymerase I, Klenow fragment of DNA polymerase I, MMLV reverse transcriptase and AMV reverse transcriptase.

9. (Previously presented) A method as in claim 1, wherein said at least one solid phase is selected from the group consisting of fiber, fibril, plastic surface, plastic bead, magnetic bead, plastic tube, gold surface, metal surface, metal bead and colloids.

10. (Currently amended) A method as in claim 1, wherein said at least one nucleotide triphosphate is selected from the group consisting of dATP, dGTP, dCTP, dUTP, dTTP, ATP, CTP, GTP, TTP, UTP inosineTP, propyne dCTP, propyne dUTP, 5-bromo dCTP, 5-iodo dUTP, 5-fluoro dUTP, 0-6 methyl dGTP, 7-deaza dGTP, N-6 methyl-2'-dATP, biotin-dATP, biotin-dCTP, biotin-dUTP, digoxigenin dUTP, digoxigenin UTP and biotin ddUTP.

11. (Currently amended) A method as in claim 1, wherein said at least one random primer is 4-70 nucleotides.

12. (Previously presented) A method as in claim 1, wherein said conditions comprise a solution with a pH between 5.5 and 9.5, a nucleotide triphosphate concentration between 1 pM and 10 mM, a Mg2+ concentration between 0.05 mM and 500 mM, and a reducing agent concentration between 0 and 500 mM, wherein the sum of the molarities is between 1 mM and 500 mM.

13. (Previously presented) A method as in claim 4, wherein said at least one ligase is selected from the group consisting of Pfu DNA ligase, T4 DNA ligase, Taq DNA ligase, T4 RNA ligase, and E. coli DNA ligase.

14. (Previously presented) A method as in claim 1, wherein said random primer is from 4 to 20 nucleotides in length.

15. (Previously presented) A method as in claim 14, wherein said at least one detectable species is selected from the group consisting of biotin, nucleic acid sequence, nucleic acid base pairing linear polymer, fluorescent molecule, electrochemiluminescent molecule, radioactive molecule, peroxidase and alkaline phosphatase.

16. (Previously presented) A method as in claim 14, wherein said at least one binding species is selected from the group consisting of biotin, antigen, lectin, ligand, hormone, nucleic acid sequence, mimitope and nucleic acid base pairing linear polymer.

17. (Previously presented) A method as in claim 14, wherein said at least one nucleic acid polymerase is selected from the group consisting of Taq DNA polymerase, Klenow fragment (3'-5') of E. coli DNA polymerase I and Klenow fragment of DNA polymerase I.

18. (Previously presented) A method as in claim 14, wherein said at least one solid phase is selected from the group consisting of magnetic bead, plastic plate and polymer bead.

19. (Previously presented) A method as in claim 14, wherein said at least one nucleotide triphosphate is selected from the group consisting of dATP, dGTP, dCTP, dUTP, dTTP, 7-deaza dGTP, biotin-dATP, biotin-dCTP, biotin-dUTP, digoxigenin dUTP, digoxigenin UTP and biotin ddUTP.

20. (Previously presented) A method as in claim 14, wherein said random primer is 6-10 nucleotides in length.

21. (Previously presented) A method as in claim 14, wherein said conditions comprise those optimal for Klenow fragment of DNA polymerase I to synthesize DNA.

22. (Previously presented) A method as in claim 20, wherein said NTP is a dNTP.

23. (Previously presented) A method for determining total nucleic acid in a sample, which comprises:

a) mixing at least one random primer at least 4 nucleotides in length having at least one detectable species, with a sample which may contain nucleic acid,

b) adding at least one nucleotide triphosphate having at least one binding species and optionally at least one second nucleotide triphosphate,

c) adding at least one nucleic acid polymerase,

d) incubating the mixture of step c), under conditions which allow said at least one nucleic acid polymerase to be active,

e) measuring total nucleic acid in said sample by measuring the total amount of said at least one detectable species or the amount of said at least one binding species, and

f) determining whether the total nucleic acid in said sample is higher or lower than a threshold amount of contamination, wherein the threshold amount of contamination is equal to or less than 100 pg.

24. (Previously presented) A method for determining total nucleic acid in a sample, which comprises:

a) mixing at least one random primer at least 4 nucleotides in length, having at least one binding species, with a sample which may contain nucleic acid,

b) adding at least one nucleotide triphosphate having at least one detectable species and optionally at least one second nucleotide triphosphate,

c) adding at least one nucleic acid polymerase,

d) incubating the mixture of step c), under conditions which allow said at least one nucleic acid polymerase to be active,

e) measuring total nucleic acid in said sample by measuring the total amount of said at least one detectable species or the amount of said at least one binding species, and

f) determining whether the total nucleic acid in said sample is higher or lower than a threshold amount of contamination, wherein the threshold amount of contamination is equal to or less than 100 pg.

25. (Previously presented) A method for determining total nucleic acid in a sample, which comprises:

a) mixing at least one random primer at least 4 nucleotides in length with a sample which may contain nucleic acid,

b) adding at least one nucleotide triphosphate having at least one binding moiety and optionally at least one second nucleotide triphosphate having at least one label and optionally at least one nucleotide triphosphate,

c) adding at least one nucleic acid polymerase,

d) incubating the mixture of step c), under conditions which allow said at least one nucleic acid polymerase to be active,

e) measuring total nucleic acid in said sample by measuring the total amount of said at least one label or the amount of said at least one binding moiety, and

f) determining whether the total nucleic acid in said sample is higher or lower than a threshold amount of contamination, wherein the threshold amount of contamination is equal to or less than 100 pg.

26. (Previously presented) A method for determining total nucleic acid in a sample, which comprises:

a) mixing at least one labeled random primer at least 4 nucleotides in length having at least one binding species and optionally at least one second random primer at least 4 nucleotides in length having at least one detectable species, with a sample nucleic acid,

b) adding at least one nucleic acid ligase,

c) incubating the mixture of step b), under conditions which allow said at least one nucleic acid ligase to be active,

d) measuring total nucleic acid in said sample by measuring the total amount of said at least one detectable species or the amount of said at least one binding species, and

e) determining whether the total nucleic acid in said sample is higher or lower than a threshold amount of contamination, wherein the threshold amount of contamination is equal to or less than 100 pg.

27. (Previously presented) A method for determining total nucleic acid in a sample, which comprises:

a) mixing at least one labeled random primer at least 4 nucleotides in length having at least one binding species and optionally at least one second random primer at least 4 nucleotides in length having at least one detectable species, with a sample which may contain nucleic acid,

b) adding at least one nucleic acid ligase and at least one nucleic acid polymerase,

c) adding at least one nucleotide triphosphate,

d) incubating the mixture of step c), under conditions which allow said at least one nucleic acid ligase and at least one nucleic acid polymerase to be active,

e) measuring total nucleic acid in said sample by measuring the total amount of said at least one detectable species or the amount of said at least one binding species, and

f) determining whether the total nucleic acid in said sample is higher or lower than a threshold amount of contamination, wherein the threshold amount of contamination is equal to or less than 100 pg.

28. (Previously presented) A method as in claim 23, wherein said at least one detectable species is selected from the group consisting of biotin, avidin, streptavidin, antibody, antigen, lectin, receptor, ligand, hormone, nucleic acid sequence, mimitope, nucleic acid base pairing linear polymer, fluorescent molecule, electrochemiluminescent molecule, radioactive molecule, colored molecule, peroxidase, alkaline phosphatase and enzymes capable of producing a detectable species.

29. (Currently amended) A method as in claim [1] 23, wherein said at least one nucleic acid polymerase is selected from the group consisting of Taq DNA polymerase, T4 DNA polymerase, Klenow fragment, Pfu DNA polymerase, Exo- Pfu DNA polymerase, E. coli DNA polymerase I, Klenow fragment of DNA polymerase I, MMLV reverse transcriptase and AMV reverse transcriptase.

30. (Previously presented) A method as in claim 23, wherein said at least one nucleotide triphosphate is selected from the group consisting of dATP, dGTP, dCTP, dUTP, dTTP, ATP, CTP, GTP, TTP, UTP inosineTP, propyne dCTP, propyne dUTP, 5-bromo dCTP, 5-iodo dUTP, 5-fluoro dUTP, 0-6 methyl dGTP, 7-deaza dGTP, N-6 methyl-2'-dATP, biotin-dATP, biotindCTP, biotin-dUTP, digoxigenin dUTP, digoxigenin UTP and biotin ddUTP.

31. (Previously presented) A method as in claim 23, wherein said at least one random primer is 4-70 nucleotides.

32. (Previously presented) A method as in claim 23, wherein said conditions comprise a solution with a pH between 5.5 and 9.5, a nucleotide riphosphate concentration between 1pM and 10mM, a Mg2+ concentration between 0.05mM and 500mM, and a reducing agent concentration between 0 and 500mM, where the sum of the molarities is between 1mM and 500mM.

33. (Previously presented) A method as in claim 26, wherein said at least one ligase is selected from the group consisting of Pfu DNA ligase, T4 DNA ligase, Taq DNA ligase, T4 RNA ligase, and E. coli DNA ligase.

34-37. (Canceled)

38. (Previously presented) A method for determining total nucleic acid in a sample, which comprises:

a) mixing at least one random primer at least 4 nucleotides in length having at least one first label, with a sample nucleic acid,

b) adding at least one nucleotide triphosphate having at least one second label and optionally at least one second nucleotide triphosphate,

c) adding at least one nucleic acid polymerase,

d) incubating the mixture of step c), under conditions which allow said at least one nucleic acid polymerase to be active,

e) measuring total nucleic acid in said sample by measuring the total amount of said at least one first label or the amount of said at least one second label, and

f) determining whether the total nucleic acid in said sample is higher or lower than a threshold amount of contamination, wherein the threshold amount of contamination is equal to or less than 100 pg.

39. (Previously presented) A method for determining total nucleic acid in a sample, which comprises:

a) mixing at least one labeled random primer at least 4 nucleotides in length having at least one first label species and optionally at least one second random primer at least 4 nucleotides in length having at least one second label, with a sample which may contain nucleic acid,

b) adding at least one nucleic acid ligase,

c) incubating the mixture of step b), under conditions which allow said at least one nucleic acid ligase to be active,

d) measuring total nucleic acid in said sample by measuring the total amount of said at least one first label or the amount of said at least one second label, and

e) determining whether the total nucleic acid in said sample is higher or lower than a threshold amount of contamination, wherein the threshold amount of contamination is equal to or less than 100 pg.

40. (Previously presented) A method for determining total nucleic acid in a sample, which comprises:

a) mixing at least one labeled random primer at least 4 nucleotides in length having at least one first label and optionally at least one second random primer at least 4 nucleotides in length having at least one second label, with a sample which may contain nucleic acid,

b) adding at least one nucleic acid ligase and at least one nucleic acid polymerase,

c) adding at least one nucleotide triphosphate,

d) incubating the mixture of step c), under conditions which allow said at least one nucleic acid ligase and at least one nucleic acid polymerase to be active,

e) measuring total nucleic acid in said sample by measuring the total amount of said at least one first label or the amount of said at least one second label, and

f) determining whether the total nucleic acid in said sample is higher or lower than a threshold amount of contamination, wherein the threshold amount of contamination is equal to or less than 100 pg.

41-61. (Canceled)

62. (Previously presented) The method of claim 1, wherein said method is capable of detecting total nucleic acid in amounts as low as 5 pg.

63. (Previously presented) The method of claim 2, wherein said method is capable of detecting total nucleic acid in amounts as low as 5 pg.

64. (Previously presented) The method of claim 3, wherein said method is capable of detecting total nucleic acid in amounts as low as 5 pg.

65. (Previously presented) The method of claim 4, wherein said method is capable of detecting total nucleic acid in amounts as low as 5 pg.

66. (Previously presented) The method of claim 5, wherein said method is capable of detecting total nucleic acid in amounts as low as 5 pg.

67. (Previously presented) The method of claim 23, wherein said method is capable of detecting total nucleic acid in amounts as low as 5 pg.

68. (Previously presented) The method of claim 24, wherein said method is capable of detecting total nucleic acid in amounts as low as 5 pg.

69. (Previously presented) The method of claim 25, wherein said method is capable of detecting total nucleic acid in amounts as low as 5 pg.

70. (Previously presented) The method of claim 26, wherein said method is capable of detecting total nucleic acid in amounts as low as 5 pg.

71. (Previously presented) The method of claim 27, wherein said method is capable of detecting total nucleic acid in amounts as low as 5 pg.

72. (Previously presented) The method of claim 38, wherein said method is capable of detecting total nucleic acid in amounts as low as 5 pg.

73. (Previously presented) The method of claim 39, wherein said method is capable of detecting total nucleic acid in amounts as low as 5 pg.

74. (Previously presented) The method of claim 40, wherein said method is capable of detecting total nucleic acid in amounts as low as 5 pg.

75-79. (Canceled)

80. (Previously presented) The method of claim 1, wherein said method is capable of detecting DNA fragments shorter than 800 basepairs.

81. (Previously presented) The method of claim 2, wherein said method is capable of detecting total DNA fragments shorter than 800 basepairs.

82. (Previously presented) The method of claim 3, wherein said method is capable of detecting total DNA fragments shorter than 800 basepairs.

83. (Previously presented) The method of claim 4, wherein said method is capable of detecting total DNA fragments shorter than 800 basepairs.

84. (Previously presented) The method of claim 5, wherein said method is capable of detecting total DNA fragments shorter than 800 basepairs.

85. (Previously presented) The method of claim 23, wherein said method is capable of detecting DNA fragments shorter than 800 basepairs.

86. (Previously presented) The method of claim 24, wherein said method is capable of detecting DNA fragments shorter than 800 basepairs.

87. (Previously presented) The method of claim 25, wherein said method is capable of detecting DNA fragments shorter than 800 basepairs.

88. (Previously presented) The method of claim 26, wherein said method is capable of detecting DNA fragments shorter than 800 basepairs.

89. (Previously presented) The method of claim 27, wherein said method is capable of detecting DNA fragments shorter than 800 basepairs.

90. (Previously presented) The method of claim 38, wherein said method is capable of detecting DNA fragments shorter than 800 basepairs.

91. (Previously presented) The method of claim 39, wherein said method is capable of detecting DNA fragments shorter than 800 basepairs.

92. (Previously presented) The method of claim 40, wherein said method is capable of detecting DNA fragments shorter than 800 basepairs.

93-97. (Canceled)

Kindly add new claims 98-132.

98. (New) A method as in claim 23, wherein said random primer is from 4 to 20 nucleotides in length.

99. (New) A method as in claim 98, wherein said at least one detectable species is selected from the group consisting of biotin, nucleic acid sequence, nucleic acid base pairing linear polymer, fluorescent molecule, electrochemiluminescent molecule, radioactive molecule, peroxidase and alkaline phosphatase.

100. (New) A method as in claim 98, wherein said at least one nucleic acid polymerase is selected from the group consisting of Taq DNA polymerase, Klenow fragment (3'-5') of E. coli DNA polymerase I and Klenow fragment of DNA polymerase I.

101. (New) A method as in claim 98, wherein said at least one nucleotide triphosphate is selected from the group consisting of dATP, dGTP, dCTP, dUTP, dTTP, 7-deaza dGTP, biotin-dATP, biotin-dCTP, biotin-dUTP, digoxigenin dUTP, digoxigenin UTP and biotin ddUTP.

102. (New) A method as in claim 98, wherein said random primer is 6-10 nucleotides in length.

103. (New) A method as in claim 98, wherein said conditions comprise those optimal for Klenow fragment of DNA polymerase I to synthesize DNA.

104. (New) A method as in claim 102, wherein said NTP is a dNTP.

105. (New) A method as in claim 2, wherein said at least one binding species is selected from the group consisting of biotin, avidin, streptavidin, antibody, antigen, lectin, receptor, ligand, hormone, nucleic acid sequence, mimitope and nucleic acid base pairing polymer.

106. (New) A method as in claim 2, wherein said at least one detectable species is selected from the group consisting of biotin, avidin, streptavidin, antibody, antigen, lectin, receptor, ligand, hormone, nucleic acid sequence, mimitope, nucleic acid base pairing polymer, fluorescent molecule, electrochemiluminescent molecule, radioactive molecule, colored molecule, peroxidase, alkaline phosphatase and enzymes capable of producing a detectable species.

107. (New) A method as in claim 2, wherein said at least one nucleic acid polymerase is selected from the group consisting of Taq DNA polymerase, T4 DNA polymerase, Klenow fragment, Pfu DNA polymerase, Exo- Pfu DNA polymerase, E. coli DNA

polymerase I, Klenow fragment of DNA polymerase I, MMLV reverse transcriptase and AMV reverse transcriptase.

108. (New) A method as in claim 2, wherein said at least one solid phase is selected from the group consisting of fiber, fibril, plastic surface, plastic bead, magnetic bead, plastic tube, gold surface, metal surface, metal bead and colloids.

109. (New) A method as in claim 2, wherein said at least one nucleotide triphosphate is selected from the group consisting of dATP, dGTP, dCTP, dUTP, dTTP, ATP, CTP, GTP, TTP, UTP inosineTP, propyne dCTP, propyne dUTP, 5-bromo dCTP, 5-iodo dUTP, 5-fluoro dUTP, 0-6 methyl dGTP, 7-deaza dGTP, N-6 methyl-2'-dATP, biotin-dATP, biotin-dCTP, biotin-dUTP, digoxigenin dUTP, digoxigenin UTP and biotin ddUTP.

110. (New) A method as in claim 2, wherein said at least one random primer is 4-70 nucleotides.

111. (New) A method as in claim 2, wherein said conditions comprise a solution with a pH between 5.5 and 9.5, a nucleotide triphosphate concentration between 1 pM and 10 mM, a Mg2+ concentration between 0.05 mM and 500 mM, and a reducing agent concentration between 0 and 500 mM, wherein the sum of the molarities is between 1 mM and 500 mM.

112. (New) A method as in claim 2, wherein said random primer is from 4 to 20 nucleotides in length.

113. (New) A method as in claim 112, wherein said at least one detectable species is selected from the group consisting of biotin, nucleic acid sequence, nucleic acid base pairing linear polymer, fluorescent molecule, electrochemiluminescent molecule, radioactive molecule, peroxidase and alkaline phosphatase.

114. (New) A method as in claim 112, wherein said at least one binding species is selected from the group consisting of biotin, antigen, lectin, ligand, hormone, nucleic acid sequence, mimitope and nucleic acid base pairing linear polymer.

115. (New) A method as in claim 112, wherein said at least one nucleic acid polymerase is selected from the group consisting of Taq DNA polymerase, Klenow fragment (3'-5') of E. coli DNA polymerase I and Klenow fragment of DNA polymerase I.

116. (New) A method as in claim 112, wherein said at least one solid phase is selected from the group consisting of magnetic bead, plastic plate and polymer bead.

117. (New) A method as in claim 112, wherein said at least one nucleotide triphosphate is selected from the group consisting of dATP, dGTP, dCTP, dUTP, dTTP, 7-deaza dGTP, biotin-dATP, biotin-dCTP, biotin-dUTP, digoxigenin dUTP, digoxigenin UTP and biotin ddUTP.

118. (New) A method as in claim 112, wherein said random primer is 6-10 nucleotides in length.

119. (New) A method as in claim 112, wherein said conditions comprise those optimal for Klenow fragment of DNA polymerase I to synthesize DNA.

120. (New) A method as in claim 118, wherein said NTP is a dNTP.

121. (New) A method as in claim 24, wherein said at least one detectable species is selected from the group consisting of biotin, avidin, streptavidin, antibody, antigen, lectin, receptor, ligand, hormone, nucleic acid sequence, mimitope, nucleic acid base pairing linear polymer, fluorescent molecule, electrochemiluminescent molecule, radioactive molecule, colored molecule, peroxidase, alkaline phosphatase and enzymes capable of producing a detectable species.

122. (New) A method as in claim 24, wherein said at least one nucleic acid polymerase is selected from the group consisting of Taq DNA polymerase, T4 DNA polymerase, Klenow fragment, Pfu DNA polymerase, Exo- Pfu DNA polymerase, E. coli DNA polymerase I, Klenow fragment of DNA polymerase I, MMLV reverse transcriptase and AMV reverse transcriptase.

123. (New) A method as in claim 24, wherein said at least one nucleotide triphosphate is selected from the group consisting of dATP, dGTP, dCTP, dUTP, dTTP, ATP, CTP, GTP, TTP, UTP inosineTP, propyne dCTP, propyne dUTP, 5-bromo dCTP, 5-iodo dUTP, 5-fluoro dUTP, 0-6 methyl dGTP, 7-deaza dGTP, N-6 methyl-2'-dATP, biotin-dATP, biotindCTP, biotin-dUTP, digoxigenin dUTP, digoxigenin UTP and biotin ddUTP.

124. (New) A method as in claim 24, wherein said at least one random primer is 4-70 nucleotides.

125. (New) A method as in claim 24, wherein said conditions comprise a solution with a pH between 5.5 and 9.5, a nucleotide riphosphate concentration between 1pM and 10mM, a Mg2+ concentration between 0.05mM and 500mM, and a reducing agent concentration between 0 and 500mM, where the sum of the molarities is between 1mM and 500mM.

126. (New) A method as in claim 24, wherein said random primer is from 4 to 20 nucleotides in length.

127. (New) A method as in claim 126, wherein said at least one detectable species is selected from the group consisting of biotin, nucleic acid sequence, nucleic acid base pairing linear polymer, fluorescent molecule, electrochemiluminescent molecule, radioactive molecule, peroxidase and alkaline phosphatase.

128. (New) A method as in claim 126, wherein said at least one nucleic acid polymerase is selected from the group consisting of Taq DNA polymerase, Klenow fragment (3'-5') of E. coli DNA polymerase I and Klenow fragment of DNA polymerase I.

129. (New) A method as in claim 126, wherein said at least one nucleotide triphosphate is selected from the group consisting of dATP, dGTP, dCTP, dUTP, dTTP, 7-deaza dGTP, biotin-dATP, biotin-dCTP, biotin-dUTP, digoxigenin dUTP, digoxigenin UTP and biotin ddUTP.

130. (New) A method as in claim 126, wherein said random primer is 6-10 nucleotides in length.

131. (New) A method as in claim 126, wherein said conditions comprise those optimal for Klenow fragment of DNA polymerase I to synthesize DNA.

132. (New) A method as in claim 130, wherein said NTP is a dNTP.